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SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANTS:

(A) NAME: Peter Stougaard
Ole Cai Hansen

(ii) TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Hunton & Williams
- (B) STREET: 1900 K Street, N.W.
- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: U.S.A.
- (F) ZIP: 20006-1109

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/669,304
(B) FILING DATE: 12 July 1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/476,910
(B) FILING DATE: 7

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Stanislaus Aksman
(B) REGISTRATION NUMBER: 28,562
(C) REFERENCE/DOCKET NO.: 54320.000003

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (202) 955-1926
- (B) TELEFAX: (202) 778-2201
- (C) TELEX: None

(1) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Tyr Glu Pro Tyr Gly Gly Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp Xaa Xaa
1 5 10 15

Xaa Gly Tyr Xaa Val Ser Ser
20

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu Xaa Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp	Ser	Glu	Gly	Asn	Asp	Gly	Glu	Leu	Phe	Xaa	Ala	His	Thr
1					5								10

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Tyr	Tyr	Phe	Lys
1			

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp	Pro	Gly	Tyr	Ile	Val	Ile	Asp	Val	Asn	Ala	Gly	Thr	Xaa	Asp
1					5				10					15

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp
1 5 10

2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Arg Asp Phe Tyr Glu Glu Met
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp Xaa Xaa
1 5 10 15

Xaa Gly Tyr Xaa Val Ser Ser
20

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu Trp Phe
1 5 10 15

2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Ser Glu Gly Asn Asp Gly Glu Leu Phe Xaa Ala His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Tyr Phe Lys
1

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Asp Pro Gly Tyr Ile Val Ile Asp Val Asn Ala Gly Thr Pro Asp
1 5 10 15

(1) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Ile Arg Asp Phe Tyr Glu Glu Met
1 5

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: modified base; N=inosine
- (B) LOCATION: base pairs 3, 6 and 12
- (C) IDENTIFICATION METHOD: commercially available
- (D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

YTNGTNGARW SNGGNTAYGA

20

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: modified base; N=inosine
- (B) LOCATION: base pairs 6 and 12
- (C) IDENTIFICATION METHOD: commercially available
- (D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AACCANARRT TNGANGCDAT NAC

23

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: modified base; N=inosine
- (B) LOCATION: base pairs 6 and 15
- (C) IDENTIFICATION METHOD: commercially available
- (D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GARGGNAAYG AYGGNGARCT NTT

23

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: modified base; N=inosine
- (B) LOCATION: base pairs 3 and 9
- (C) IDENTIFICATION METHOD: commercially available
- (D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AANAGYTCNC CRTCRTTNCC YTC

23

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATTGGGGCTC CTTCAAGACC TT

22

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGATGATTCC AAAGTTTC

18

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGGAAGAAT ACGGTTGG

18

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TACTATTCG TCTGCTTGGG

20

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAACTCTTCC GTGGTCTCCT

20

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCACCTGCGT GTTGGGGTCT

20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CAGATCTACA AAACATGCGA G

21

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGTCGCAGAC TGTACTTG

18

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAGTGTACAC GACATAAA

18

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATGGCTACTC TTCCCCAGAA AG

22

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 84..1721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TGAATTCGTG GGTGAAAGAG CCCTTGCCT CGTCTCTCTG GTACCGTGTG TGTCAAAGGT 60

TCGCTTGCAC ACTGAACCTTC ACG ATG GCT ACT CTT CCT CAG AAA GAC CCC 110
 Met Ala Thr Leu Pro Gln Lys Asp Pro
 1 5

GGT TAT ATT GTA ATT GAT GTC AAC GCG GGC ACC GCG GAC AAG CCG GAC 158
 Gly Tyr Ile Val Ile Asp Val Asn Ala Gly Thr Ala Asp Lys Pro Asp
 10 15 20 25

CCA CGT CTC CCC TCC ATG AAG CAG GGC TTC AAC CGC CGC TGG ATT GGA 206
 Pro Arg Leu Pro Ser Met Lys Gln Gly -Phe Asn Arg Arg Trp Ile Gly
 30 35 40

ACT AAT ATC GAT TTC GTT TAT GTC GTG TAC ACT CCT CAA GGT GCT TGT 254
 Thr Asn Ile Asp Phe Val Tyr Val Val Tyr Thr Pro Gln Gly Ala Cys
 45 50 55

ACT GCA CTT GAC CGT GCT ATG GAA AAG TGT TCT CCC GGT ACA GTC AGG 302
 Thr Ala Leu Asp Arg Ala Met Glu Lys Cys Ser Pro Gly Thr Val Arg
 60 65 70

ATC GTC TCT GGC GGC CAT TGC TAC GAG GAC TTC GTA TTT GAC GAA TGC 350
 Ile Val Ser Gly Gly His Cys Tyr Glu Asp Phe Val Phe Asp Glu Cys
 75 80 85

GTC AAG GCC ATC ATC AAC GTC ACT GGT CTC GTT GAG AGT GGT TAT GAC	398
Val Lys Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp	
90 95 100 105	
GAC GAT AGG GGT TAC TTC GTC AGC AGT GGA GAT ACA AAT TGG GGC TCC	446
Asp Asp Arg Gly Tyr Phe Val Ser Ser Gly Asp Thr Asn Trp Gly Ser	
110 115 120	
TTC AAG ACC TTG TTC AGA GAC CAC GGA AGA GTT CTT CCC GGG GGT TCC	494
Phe Lys Thr Leu Phe Arg Asp His Gly Arg Val Leu Pro Gly Gly Ser	
125 130 135	
TGC TAC TCC GTC GGC CTC GGT GGC CAC ATT GTC GGC GGA GGT GAC GGC	542
Cys Tyr Ser Val Gly Leu Gly His Ile Val Gly Gly Asp Gly	
140 145 150	
ATT TTG GCC CGC TTG CAT GGC CTC CCC GTC GAT TGG CTC AGC GGC GTG	590
Ile Leu Ala Arg Leu His Gly Leu Pro Val Asp Trp Leu Ser Gly Val	
155 160 165	
GAG GTC GTC GTT AAG CCA GTC CTC ACC GAA GAC TCG GTA CTC AAG TAT	638
Glu Val Val Val Lys Pro Val Leu Thr Glu Asp Ser Val Leu Lys Tyr	
170 175 180 185	
GTG CAC AAA GAT TCC GAA GGC AAC GAC GGG GAG CTC TTT TGG GCA CAC	686
Val His Lys Asp Ser Glu Gly Asn Asp Gly Glu Leu Phe Trp Ala His	
190 195 200	
ACA GGT GGC GGT GGC GGA AAC TTT GGA ATC ATC ACC AAA TAC TAC TTC	734
Thr Gly Gly Gly Asn Phe Gly Ile Ile Thr Lys Tyr Tyr Phe	
205 210 215	
AAG GAT TTG CCC ATG TCT CCA CGG GGC GTC ATC GCA TCA AAT TTA CAC	782
Lys Asp Leu Pro Met Ser Pro Arg Gly -Val Ile Ala Ser Asn Leu His	
220 225 230	
TTC AGC TGG GAC GGT TTC ACG AGA GAT GCC TTG CAG GAT TTG TTG ACA	830
Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr	
235 240 245	
AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG	878
Lys Tyr Phe Lys Leu Ala Arg Cys Asp Trp Lys Asn Thr Val Gly Lys	
250 255 260 265	
TTT CAA ATC TTC CAT CAG GCA GCG GAA GAG TTT GTC ATG TAC TTG TAT	926
Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr	
270 275 280	

ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC	974
Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His	
285 290 295	
TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC	1022
Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro	
300 305 310	
ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG GCG CCG TTC CCC GTG CGG	1070
Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg	
315 320 325	
CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG	1118
Pro Arg Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr	
330 335 340 345	
ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC GGC TCC GGG	1166
Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly	
350 355 360	
CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAG GAT TTC	1214
Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe	
365 370 375	
CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG	1262
Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro	
380 385 390	
GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC	1310
Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp	
395 400 405	
ATG TTT GGT GGT GAG ATT CAC AAG GTG GTC TGG GAT GCG ACG GCA GTC	1358
Met Phe Gly Gly Glu Ile His Lys Val Val Trp Asp Ala Thr Ala Val	
410 415 420 425	
GCG CAG CGC GAG TAC ATC ATC AAA CTG CAG TAC CAG ACA TAC TGG CAG	1406
Ala Gln Arg Glu Tyr Ile Ile Lys Leu Gln Tyr Gln Thr Tyr Trp Gln	
430 435 440	
GAA GAA GAC AAG GAT GCA GTG AAC CTC AAG TGG ATT AGA GAC TTT TAC	1454
Glu Glu Asp Lys Asp Ala Val Asn Leu Lys Trp Ile Arg Asp Phe Tyr	
445 450 455	
GAG GAG ATG TAT GAG CCG TAT GGC GGG GTT CCA GAC CCC AAC ACG CAG	1502
Glu Glu Met Tyr Glu Pro Tyr Gly Gly Val Pro Asp Pro Asn Thr Gln	
460 465 470	

GTG GAG AGT GGT AAA GGT GTG TTT GAG GGA TGC TAC TTC AAC TAC CCG	1550
Val Glu Ser Gly Lys Gly Val Phe Glu Gly Cys Tyr Phe Asn Tyr Pro	
475 480 485	
GAT GTG GAC TTG AAC AAC TGG AAG AAC GGC AAG TAT GGT GCC CTC GAA	1598
Asp Val Asp Leu Asn Asn Trp Lys Asn Gly Lys Tyr Gly Ala Leu Glu	
490 495 500 505	
CTT TAC TTT TTG GGT AAC CTG AAC CGC CTC ATC AAG GCC AAA TGG TTG	1646
Leu Tyr Phe Leu Gly Asn Leu Asn Arg Leu Ile Lys Ala Lys Trp Leu	
510 515 520	
TGG GAT CCC AAC GAG ATC TTC ACA AAC AAA CAG AGC ATC CCT ACT AAA	1694
Trp Asp Pro Asn Glu Ile Phe Thr Asn Lys Gln Ser Ile Pro Thr Lys	
525 530 535	
CCT CTT AAG GAG CCC AAG CAG ACG AAA TAGTAGGTCA CAATTAGTCA	1741
Pro Leu Lys Glu Pro Lys Gln Thr Lys	
540 545	

TCGACTGAAG TGCAGCACTT GTCGGATACG GCGTGATGGT TGCTTTTAT AAACTTGGTA 1801

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ala Thr Leu Pro Gln Lys Asp Pro	Gly	Tyr Ile Val Ile Asp Val	
1	5	10	15

Asn Ala Gly Thr Ala Asp Lys Pro Asp Pro	Arg	Leu Pro Ser Met Lys
20	25	30

Gln Gly Phe Asn Arg Arg Trp Ile	Gly	Thr Asn Ile Asp Phe Val Tyr
35	40	45

Val Val Tyr Thr Pro Gln Gly Ala Cys Thr	Ala	Leu Asp Arg Ala Met
50	55	60

Glu Lys Cys Ser Pro Gly Thr Val Arg Ile	Val	Ser Gly Gly His Cys	
65	70	75	80

Tyr Glu Asp Phe Val Phe Asp Glu Cys Val	Lys	Ala Ile Ile Asn Val
85	90	95

Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val
 100 105 110

Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp
 115 120 125

His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly
 130 135 140

Gly His Ile Val Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly
 145 150 155 160

Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val
 165 170 175

Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly
 180 185 190

Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Asn
 195 200 205

Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro
 210 215 220

Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr
 225 230 235 240

Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg
 245 250 255

Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala
 260 265 270

Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala
 275 280 285

Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile
 290 295 300

Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His
 305 310 315 320

Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser
 325 330 335

Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala
 340 345 350

Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr
 355 360 365

Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val
 370 375 380
 Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu
 385 390 395 400
 Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His
 405 410 415
 Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile
 420 425 430
 Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val
 435 440 445
 Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr
 450 455 460
 Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val
 465 470 475 480
 Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
 485 490 495
 Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
 500 505 510
 Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
 515 520 525
 Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
 530 535 540
 Thr Lys
 545

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACCAAGTTA TAAAAAGCAA CCATCAC

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATGAATTCGT GGGTCGAAGA GCCC

24

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAGGAATTCA TATGGCTACT CTTCCCCAGA AAG

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